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A. DeClaw
RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/147,443BDATE: 01/25/2001
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3 <110> APPLICANT: Morell, Andreas
 4 Imboden, Martin
 5 Stadler, Beda
 6 Miescher, Sylvia
 7 Vogel, Monique
 8 Amstutz, Hanspeter
 10 <120> TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
 11 STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
 12 THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
 13 PREPARATION AND USE
 15 <130> FILE REFERENCE: 6816/P63221US0
 17 <140> CURRENT APPLICATION NUMBER: 09/147,443B
 18 <141> CURRENT FILING DATE: 1999-01-21
 20 <150> PRIOR APPLICATION NUMBER: PCT/EP97/03253
 21 <151> PRIOR FILING DATE: 1997-06-20
 23 <150> PRIOR APPLICATION NUMBER: EP 96810421.6
 24 <151> PRIOR FILING DATE: 1996-06-24
 26 <160> NUMBER OF SEQ ID NOS: 64
 28 <170> SOFTWARE: PatentIn Ver. 2.1
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 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
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 36 <221> NAME/KEY: CDS
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 42 1 5 5 10 15
 44 tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat 30
 45 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 144
 46 20 25 30
 48 gcc atg cac tgg qtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 45
 49 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 192
 50 35 40 45
 52 gca ggt ata tgg ttt gat gga aqt aac aaa aac tat gca gac tcc gtg 55 240
 53 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 60
 54 50 55 60
 56 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 75 288
 57 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80
 58 65 70 75
 60 ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat tgt 90 336
 61 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 95
 62 85
 64 gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac atg 65 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met

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85	35 40 45 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	50		
86	55 60 65 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys	70 75	80	
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119	19 25 30 Gtc Acc Atc Act Tgc Cgg Gca Agt Cag Agc Att Agg Agc Cat Ttg Aat	35		
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121	50 55 60 Tgg Tat Cag Cag AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT	65		144
123	65 70 75 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly	80		
124	75 80 85 Gcg Tcc Act Ttg Caa Agt Ggc Gtc Cca Tca Agg Ttc Agt Ggc Agt Ggc	90		192
127	90 95 100 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	105		
128	100 105 110 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	115		
129	110 115 120 Tct Ggg Gca Gtt Ttc Act Ctc Acc Atc Gcc Agt Cta Caa Cct Gaa Gat	125		240
131	125 130 135 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp	135		
132	135 140 145 Ttt Gca Act Tac Tac Tgt Caa Gag Agt Tac Agt Aat Cct Cta Atc Acc	150	155	288

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156 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
157 35 40 45
159 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
160 50 55 60
162 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
163 65 70 75 80
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187 tcc ctg aga ctc tcc tgt gaa gca gct ttc gca ctc aga agt tct
188 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
189 20 25 30 144
191 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg
192 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
193 35 40 45 192
195 gca ctt ata tgg ttt gat gga agt atc aga tcc tat gca gaa tcc gtg
196 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
197 50 55 60 240
199 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
201 65 70 75 80 288
203 ctc caa atg cgc agt ctg agt gcc gac gac gct gtg tat tac tgt
204 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys

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205 207 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg
208 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
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225 20 25 30
226 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
227 35 40 45
228 40 45
229 50 55 60
230 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
231 55 60
232 60 65 70 75 80
233 70 75 80
234 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
235 85 90 95
236 90 95
237 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
238 85 90 95
239 95 100 105 110
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256 20 25 30 96
257 25 30 35 44
258 35 40 45 144
259 40 45 50 192
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275 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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278 ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act
279 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
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300 35 40 45
302 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
303 50 55 60
305 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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331 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
332 20 25 30 96
334 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg
335 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
336 35 40 45 144
338 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg
339 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
340 50 55 60 192
342 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat
343 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
288 318 95 318 48 96 144 240 192

VERIFICATION SUMMARY
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